

FIG. 1

Human glycoprotein hormone  $\beta 10$  polypeptide:

MKLAFLGLPMALLLAGYGCVLGASSGNLRTFVGCAVREFTFLAKKPGCRGLRITTDACWGR CET  

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WEKPILEPPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGACSTATTECETI

Nucleic acid encoding human glycoprotein hormone  $\beta 10$  polypeptide:

ATGAAGCTGGCATTCCTCTTCCTTGGCCCCCATGGCCCTCCTCCTTCTGGC  
TGGCTATGGCTGTGTCCTCGGTGCTCCAGTGGGAACCTGGGCACCTTTG  
TGGCTGTGCCGTGAGGGAGTTACTTTCCTGGCCAAAGAACGAGCTGC  
AGGGCCTTCGGATCACACGATGCCTGCTGGGTCGCTGTGAGACCTG  
GGAGAAACCCATTCTGGAACCCCTATATTTGAAGCCCATCATCGAGTCT  
GTACCTACACGAGACCAACAGGTGACTGTCAAGTGCCCAACTGTGCC  
CCGGAGTCGACCCCTTCTACACCTATCCCGTGGCCATCCGCTGTGACTG  
CGGAGCCTGCTCCACTGCCACCCACGAGTGTGAGACCATCTGAGGCCGCT  
AGCTGCTCTCTGCAGACCCACCTGTGTGAGCAGCACATGC

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## FIG. 2A

GAP OF: HUMAN TSH- $\beta$  CHECK: 4247 FROM: 1 TO: 118

TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

### SYMBOL COMPARISON TABLE:

/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP

COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003

QUALITY:	140	LENGTH:	129
RATIO:	1.321	GAPS:	4
PERCENT SIMILARITY:	47.368	<b>PERCENT IDENTITY:</b>	<b>36.842</b>

### MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

	=	IDENTITY
:	=	2
.	=	1

HUMAN TSH- $\beta$  X HUMAN  $\beta$ 10

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1 .....FCIPTEYTMHIERRECA YCLTINTTICAGYCMTRDINGKL 40
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWE..KPI 47

41 FLPKYALSQD.VCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGKCN 89
      |  |  .  ||||  :  ||.:|  |  |  |  |  |  |  |  |  |
48 LEPPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGACS 97

90 TDYSDCIHEAIAKTN YCTKPQKSYLVGFSV 118
      |  .:|  |  |
98 TATTEC..ETI..... 106
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## FIG. 2B

GAP OF: HUMAN FSH- $\beta$  CHECK: 8841 FROM: 1 TO: 111  
TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	156	LENGTH:	122
RATIO:	1.472	GAPS:	3
PERCENT SIMILARITY:	44.211	<b>PERCENT IDENTITY:</b>	<b>35.789</b>

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):  
| = IDENTITY  
: = 2  
. = 1

HUMAN FSH- $\beta$  X HUMAN  $\beta$ 10

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1 .....NSCELTNITIAIEKEECRFCISINTTWCAGYCYTRDL.VYK 40
      | . | . | | : | | | | | : : .
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE 49

41 DPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTPVATQCHCGKCDSD 90
      | : ||: | ||: . | || | | | | . | || | .
50 PPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGACSTA 99

91 STDC.TVRGLGPSYCSFGEMKE 111
      .|:| |:
100 TTECETI..... 106

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## FIG. 2C

GAP OF: HUMAN LH- $\beta$  CHECK: 5679 FROM: 1 TO: 121

TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	140	LENGTH:	125
RATIO:	1.321	GAPS:	3
PERCENT SIMILARITY:	44.118	<b>PERCENT IDENTITY:</b>	<b>32.353</b>

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

	=	IDENTITY
:	=	2
.	=	1

HUMAN LH- $\beta$  X HUMAN  $\beta$ 10

1	.SREPLRPW..CHPINAILAVEKEGCPVCITVNTTICAGYCPTMMR.VLQ	46
	.   .     : :         : :   :	
1	ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE	49
47	AVLPPLPQVVCTYRDVRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRS	96
	: : . :             . :       :       .	
50	PPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYTPVAIRCDCGACSTA	99
97	TSDCGGPKDHPLTCDHPQLSGLLFL	121
	. :	
100	TTECETI.....	106

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## FIG. 2D

GAP OF: HUMAN CG- $\beta$  CHECK: 2358 FROM: 1 TO: 145

TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	131	LENGTH:	149
RATIO:	1.236	GAPS:	3
PERCENT SIMILARITY:	42.157	<b>PERCENT IDENTITY:</b>	<b>31.373</b>

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

| = IDENTITY  
: = 2  
. = 1

HUMAN CG- $\beta$  X HUMAN  $\beta$ 10

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1  .SKEPLRP..RCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTR.VLQ 46
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1  ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE 49

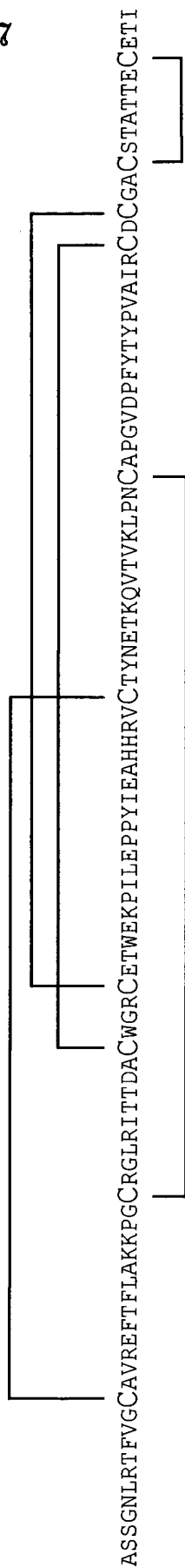
47  GVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRS 96
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
50  PPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGACSTA 99

97  TTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ 145
   |  |  |
100 TTECETI..... 106
```

FIG. 3

human  $\beta$ 10

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— = Disulfide bond

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## FIG. 4

BESTFIT of: human  $\beta$ 10 check: 6611 from: 1 to: 106

to: mouse  $\beta$ 10 check: 7740 from: 1 to: 106

Symbol comparison table: blosum62.cmp CompCheck: 6430  
BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl. Acad.  
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003

Quality:	577	Length:	106
Ratio:	5.443	Gaps:	0
Percent Similarity:	97.170	Percent Identity:	93.396

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

human  $\beta$ 10 x mouse  $\beta$ 10

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1 ASSGNLRTFVGCAVREFTFLAKKPGCRGLRITTDACWGRCEWKEPIL 50
. ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 SSSGNLHTFVGCAVREFTFMAKKPGCRGLRITTDACWGRCEWKEPIL 50

51 PYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTPVAIRCDGACSTAT 100
||| |: ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 PYIEAYHRVCTYNETRQVTVKLPNCAPGVDPFYTPMAVRCDGACSTAT 100

101 TECETI 106
||| |
101 TECETI 106

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